

GENE PRECURSOR-SEQUENCE P-SEQID GENE-SEQ G-SEQID FOLDED PRECURSOR

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GAM15 CAATGAGTCCGAGATCTTC 1 TGAGTCCGAG 16 GA GAG-- AGA T
GACCTGGAGGAGGAGATATG ATCTTCAGAC CAAT GTCC ATCTTC CC G
AGGGACAATTG CTGG ||||| ||||| |||
GTTA CAGG TAGAGG GG G
A- GAGTA A-- A

GAM16 CATATGTATGTTCAAGGGAA 2 TTTTATAGAC 17 - T CAGGG GG
AGCTAGGGGATGGTTTATA ATCACTATG CATA TG ATGTTT AAAGCTA G
GACATCACTATG ||||| ||||| |||||
GTAT AC TACAGA TTTTGTT /
C - TA-- AG

GAM17 CCACTCTATTTGTGCATCA 3 TATGATACAG 18 CTC T ----- G T
GATGCTAAAGCATATGATAC AGGTACATAA CCA TATT TGTGC ATCA ATGC A
AGAGGTACATAATGTTGG TGTT ||||| ||||| |||||
GGT GTAA ACATG TAGT TACG A
TT- T GAGACA A A

GAM18 CCATAATGATGCAGAGAGGC 4 TTAAGTGT 19 - T GAGA AGGAA
AATTTAGGAACCAAAGAAA CAATTGTGG CCATAAT GA GCA GGCAATT C
GATTGTTAACGTGTTCAATT ||||| |||||
GTGG GGTGTTA CT TGT TTGTTAGAA C
A T GAA- AGAAA

GAM19 CCATTGACAGAAGAAAAAT 5 TGACAGAAGA 20 --- - AGAAAAAA AA
AAAAGCATTAGTAGAAATT AAAAATAAAA CCAT TG ACAGA TAA G
GTACAGAGATGG GCAT ||||| |||||
GGTA AC TGT 20 ATT /
GAG A AAAGATG- AC

GAM20 CCTCTATTGTGTGCATCAA 6 TATTGTGTGC 21 G ----- A AAA ATAGAGA
GGATAGAGATAAAAGACACC ATCAAAGGAT CCTCTATT TGT GC TC GG T
AAGGAAGCTTAGACAAGAT AGAG ||||| ||| |||||
AGAGG GGAGATAG ACA CG AG CC A
A GATT A GAA ACAGAAA

GAM21 GAATAGTTTGCTGTACTT 7 TAGTTTTGC 22 G GTACT AG
TCTATAGTGAATAGAGTTAG TGTACTTTCT GAATA TTTTGCT TTCTAT T
GCAGGGATATTCA TAG ||||| |||||
CTTAT AGGGACGG GAGATA /
- ATT-- AG

GAM22 GCCACATACCTAGAAGAATA 8 TAAGATGGGT 23 A--- GAAGAATA A - G
AGACAGGGCTTGAAAGGAT GGCAAGTGGT GCCAC TACCTA AG CAGGG CTT G
TTTGCATAAGATGGGTGGC ||||| ||||| |||||
AAGTGGT TGGTG GTGGGT TC GTTTT GGA A
AACG AGAATA-- - A A

GAM23 GGAGACAGCGACGAAGAGCT 9 CAGACTCATC 24 C GAC A - C CAG
CATCAGAACAGTCAGACTCA AAGCTTCTCT GGAGA AGC GA GAG CT AT A
TCAAGCTTCTCT ||||| ||||| |||||
TCTCT TCG CT CTC GA TG /
- AA- A A C ACA

GAM24 GGTCCAAAATGCGAACCCAG 10 TCCAAAATGC 25 AA GAACCC TTA
ATTGTAAGACTATTTAAAA GAACCCAGAT GGTCC AATGC AGAT G A
GCATTGGGACC TGTA ||||| ||||| |||||
CCAGG TTACG TTTA C /
G- AAAAT- TAG

GAM25 GTACTGGGTCTCTCTGGTTA 11 TCTCTGGTTA 26 C C A TCT CT
GACCAGATCTGAGCCTGGGA GACCAGATCT GTA TGGGT TCTCTGGTTAG CCAGA GAGC G
GCTCTGGCTAACTAGGGA GAGC ||||| ||||| |||||
ACCCACTGC CGT ACCCA AGGGATCAATC GGTCT CTCG G
C - - --- AG

GAM26 TAATTGGAAGAAATCTGTTG 12 TTGGTTGCAC 27 T ----- TT
ACTCAGATTGGTTGCACTTT TTTAAATTT TAAT GGAAGA AATCTG G
AAATTTCCCATTA CCCA ||||| |||||
ATTA CCTTT TTAGAC A
C AAATTCACGTTGG TC

GAM27 TCTTGCGAACGACCCCTCG 13 TGGCAACGAC 28 CAACGA CG ACA
TCACAATAAGATAGGGGGG CCCTCGTCAC TCTTG G CCCCT TC A
CAACTAAAGG AATA ||||| |||||
GGAAATC GGGGG AG T
AACG-- AT AAA

GAM28 TTACCCATAGTGCAGAAC 14 TATAGTGCAG 29 TATA GAACA-- C GGCAA ACA
TCCAGGGGCAAATGGTACAT AACATCCAGG TTACCC GTGCA TC AGG ATGGT T
CAGGCCATATCACCTAGAAC GGCA ||||| ||||| |||||
TTAAATGCATGGTAA AATGGG TACGT AG TCC TACCG /
---- AAATTC A ACTA- GAC

GAM29 TTCATTGCCAAGTTGTTTC 15 AGCCTTAGGC 30 A AG----- T
ATAACAAAAGCCTAGGCAT ATCTCCTATG TTC TTGCCA TTTGTT C
CTCCTATGGCAGGAA GCAG ||||| |||||
AAG GACGGT AAACAA A
- ATCCTCTACGGATTCCGA T

GENE	TARGET	UTR SEQUENCE	SEQID	BINDING-SITE
GAM15	PRIM2A	3' CAGGCAGATCTCAGACTC GAGTC GAGATCT CTCAG CTCTAGA A C ____	50	C TCAGA CCTG GGAC
GAM15	RAP1B	3' CCAGGTCTGAAGAACGTGGCC CA TG GT AG TCTTCAGACCTGG AC CG TC AGAACGCTGGACC C TTG A	142	A CCG A
GAM15	RET	3' CCAGGTCTAAACAGCTGACCCA TG GTC AG AGACCTGG AC CAG TC TCTGGACC C __ GACAAA	173	A CG ATCTTC
GAM15	RET	3' CCAGGTCTAAACAGCTGACCCA TG GTC AG AGACCTGG AC CAG TC TCTGGACC C __ GACAAA	174	A CG ATCTTC
GAM15	RET	3' CCAGGTCTAAACAGCTGACCCA TG GTC AG AGACCTGG AC CAG TC TCTGGACC C __ GACAAA	179	A CG ATCTTC
GAM15	RET	3' CCAGGTCTAAACAGCTGACCCA TG GTC AG AGACCTGG AC CAG TC TCTGGACC C __ GACAAA	37	A CG ATCTTC
GAM15	AMOTL1	3' CTGATAAAAGATTCTAGACTCA TGAGTC GAGATCT TCAG ACTCAG CTTAGA AGTC A AAT	304	C ____
GAM15	DGKZ	3' CCAGACCTAGGGCTGGACTCA TGAGTCC AG TCTT AG CTGG ACTCAGG TC GGGG TC GACC _ _ _ CA	70	G A C AC
GAM15	DKFZP586G1122	3' CAGGTCTAGCCGGGCCA TG GTCCG CT AGACCTG AC CGGGC GA TCTGGAC C C ____	265	A AGAT TC
GAM15	FLJ22127	3' CCAGGCCTGAATGGATGGACTC A TGAGTCC ATCT TCAG CCTGG 	192	GAG ____ A

ACTCAGG TAGG AGTC GGACC
_____ TA C
GAM15 LOC126248 3' CAGCCCTGGCTGGACTC 308 G ATCT AC _
GAGTCC AG TCAG CT G
|||||| || |||| |||
CTCAGG TC GGTC GA C
_ _____ CC A
GAM15 LOC146640 5' CCAGGTGACCTACCCGGACTCA 323 AGATCT AG
TGAGTCCG TC ACCTGG
|||||| || |||||
ACTCAGGC AG TGGACC
CCATCC __
GAM15 LOC153416 3' CCAGGTCTGAAGAACTGTTGCC 263 A CCG A
CA TG GT AG TCTTCAGACCTGG
|| || || |||||||||
AC CG TC AGAAGTCTGGACC
C TTG A
GAM15 LOC220790 3' CCAGGTCTGAAGAACTGTTGCC 378 A CCG A
CA TG GT AG TCTTCAGACCTGG
|| || || |||||||||
AC CG TC AGAAGTCTGGACC
C TTG A
GAM16 PRKG2 3' CATGGTGGTATCTAAAAA 103 T C
TTTTA AGA ATCACTATG
|||||| |||||||
AAAAT TCT TGGTGGTAC
_ A
GAM16 AFAP 3' CATAGCAGGGCGTCTGTAAAA 183 A_ A_
TTTTATAGAC TC CTATG
|||||| || |||||
AAAATGTCTG GG GATAC
CG AC
GAM16 C3AR1 3' CATAGTGAAAGTTATAAGA 76 A_
TTTTATAGAC TC ACTATG
|||||| |||||||
AGAATATTG AGTGATAC
AA
GAM16 FLJ22029 3' CATGAAAATGTCTATAGAA 203 CAC
TTTTATAGACAT TATG
|||||| |||||
AAGATATCTGTA GTAC
AAA
GAM16 SEMA5A 3' CATAGTGACGTCCCTGAAGA 72 ATA A
TTTT GAC TCACTATG
||| || |||||
AGAA CTG AGTGATAC
GTC C
GAM16 UNC5D 3' CATAGGATTCTATAGAA 234 C A
TTTTATAGA ATC CTATG
|||||| |||||

AAGATATCT TAG GATAC
T _
GAM16 LOC129446 3' CATAGAATGTGTCTATAAA 315 CA_
TTTATAGACAT CTATG
||||||| |||||
AAATATCTGTG GATAC
TAA

GAM16 LOC153396 3' CATACTGGCTGCCTATAGAA 338 A _
TTTTATAG CA TCACTATG
||||||| |||||
AAGATATC GT GGTGATAC
C C

GAM16 LOC50999 3' CATAATGGTGTCTTAAAAA 145 T C
TTTTA AGACATCA TATG
||||| ||||| |||||
AAAAT TCTGTGGT ATAC
— A

GAM17 KIAA0830 3' AACATTATGCTTACTGCATC 290 A _ TA
GAT CAG AGG CATAATGTT
||| ||||| |||||
CTA GTC TTC GTATTACAA
C A _

GAM17 PREI3 3' AACATTATGTACTGTATATAC 275 CAGA_
AT ATGATA GGTACATAATGTT
||||| ||||| |||||
TACTAT TCATGTATTACAA
ATATG

GAM17 SEC15L 3' ACATATGCCTCTACTCATA 297 TAC CATA
TATGA AGAGGTA ATGT
||||| ||||| |||||
ATACT TCTCCGT TACA
CA_ A__

GAM17 LOC152317 3' AACATCAATGGACTCTGTATCA 352 GTA A_
TGATACAGAG CAT ATGTT
||||||| |||||
ACTATGTCTC GTA TACAA
AG_ AC

GAM18 DSCR1 3' CATTGGAAATACTTAA 81 TT
TTAAGTGTTCAA GTG
||||||| |||||
AATTCATAAAGTT TAC
T_

GAM18 ELMO2 3' CCAGGAGAACACTTA 235 AA G
TAAGTGTTC TT TGG
||||||| |||||
ATTCACAAAG AG ACC
— G

GAM18 ELMO2 3' CCAGGAGAACACTTA 186 AA G
TAAGTGTTC TT TGG
||||||| |||||

			ATT CACAAAG AG ACC		
			__ G		
GAM18	FGF5	3'	CCACAGGGAGCAAACACTTAG	227	CAA__
			TTAAGTGT TTT	TTGTGG	
			GATTCACAAA	GACACC	
			CGAGG		
GAM18	FGF5	3'	CCACAGGGAGCAAACACTTAG	83	CAA__
			TTAAGTGT TTT	TTGTGG	
			GATTCACAAA	GACACC	
			CGAGG		
GAM18	NEFH	3'	CCACACGTAAACACTTGA	180	CAAT
			TTAAGTGT TTT	TGTGG	
			AGTTCACAAA	ACACC	
			TGC__		
GAM18	NFIB	3'	CCACAAAAGAACACTTAA	93	AA
			TTAAGTGT TTT C	TTGTGG	
			AATTCACAAAG	AACACC	
			AA		
GAM18	PRKY	3'	CCATAAATGAAACACTTGA	62	A
			TTAAGTGT TTT CA	TTGTGG	
			AGTTCACAAAGT	AATACC	
			A		
GAM18	RNF18	5'	CCACAATTGGGTTCTTA	172	TGT
			TAAG	TTCAATTGTGG	
			ATTC	GGGTTAACACC	
			TT__		
GAM18	SLC1A3	3'	CCACAATTGAAATT TTT AA	77	T
			TTAAG	GTTCAATTGTGG	
			AATTT TAAAGTTAACACC		
			T		
GAM18	VMD2	3'	CCATTGGAAACATTAA	78	AATT
			TTAAGTGT TTT C	GTGG	
			AATTTACAAAG	TACC	
			GT__		
GAM18	XRCC3	5'	CCAGGGAGACACTTAA	91	AAT G
			TTAAGTGT TTT C	T TGG	
			AATTCACAGAG	G ACC	
			__ G		
GAM18	ARHGAP5	3'	CTATATGAAACATTAA	321	AT
			TTAAGTGT TTT CA	TGTGG	

AATTTACAAAGT ATATC

GAM18 EFA6R 3' CCATTGTGAAACACTTAA 140 ATT
TTAAGTGTTCAGTGG
||||||| ||||
AATTCACAAAGT TACC
GT_

GAM18 KIAA0903 3' CCACATGTAACACTTA 294 T AT
TAAGTGTTCA TGTGG
||||||| |||||
ATTCACAA GT ACACC
T _

GAM18 KIAA1244 3' CCACAATTGTCTGAACAT 295 _____
GTGTTT CAATTGTGG
||||| |||||||
TACAAG GTTAACACC
TCT

GAM18 Rpo1-2 3' CTGTGGTAAGAACACTTAA 214 CA TG
TTAAGTGTTC AT TGG
||||||| || |||
AATTCACAAAG TG GTC
AA GT

GAM18 LOC115574 3' CCACAACTGGAAACACTTGA 303 AA_
TTAAGTGTTC TTGTGG
||||||| |||||
AGTTCACAAAG AACACC
GTC

GAM18 LOC144144 5' CCACAATTGGGTTCTTA 260 TGT
TAAG TTCAATTGTGG
||| |||||||
ATTC GGGTTAACACC
TT_

GAM18 LOC148254 3' CCATCAAAGAACACTTAA 329 AA _
TTAAGTGTTC TTG TGG
||||||| |||||
AATTCACAAAG AAC ACC
AA T

GAM18 LOC157624 5' CCACTGAAACATTAA 359 ATT
TTAAGTGTTCAGTGG
||||||| |||||
AATTTACAAAGT CACC

GAM18 LOC220486 5' CCACAATTGGGTTCTTA 374 TGT
TAAG TTCAATTGTGG
||| |||||||
ATTC GGGTTAACACC
TT_

GAM19 AGL 3' ATGCTTTCATTTTTCACTG 31 AA A
CAG GAAAAAAT AAAGCAT
||| |||||||

			GTC	CTTTTTTA	TTTCGTA			
			A_	C				
GAM19	AGL	3'	ATGCTTCATTTTTCACTG	43	AA	A		
			CAG	GAAAAAAT	AAAGCAT			
			GTC	CTTTTTTA	TTTCGTA			
			A_	C				
GAM19	AGL	3'	ATGCTTCATTTTTCACTG	44	AA	A		
			CAG	GAAAAAAT	AAAGCAT			
			GTC	CTTTTTTA	TTTCGTA			
			A_	C				
GAM19	AGL	3'	ATGCTTCATTTTTCACTG	45	AA	A		
			CAG	GAAAAAAT	AAAGCAT			
			GTC	CTTTTTTA	TTTCGTA			
			A_	C				
GAM19	AGL	3'	ATGCTTCATTTTTCACTG	46	AA	A		
			CAG	GAAAAAAT	AAAGCAT			
			GTC	CTTTTTTA	TTTCGTA			
			A_	C				
GAM19	AGL	3'	ATGCTTCATTTTTCACTG	47	AA	A		
			CAG	GAAAAAAT	AAAGCAT			
			GTC	CTTTTTTA	TTTCGTA			
			A_	C				
GAM19	ALB	5'	GCTTTCTCTTGTCA	40	AAAAAT			
			TGACAGAAGA	AAAAGC				
			ACTGTCTTCT	TTTCG				
			C_____					
GAM19	CKN1	3'	TTTTATTCTTCTTCA	32	C	A		
			TGA	AGAAGAAA	AATAAAA			
			ACT	TCTTCTTT	TTATTT			
			—	C				
GAM19	HHIP	3'	TTTATTTTTATCCTGTCA	189	AAG			
			TGACAG	AAAAAATAAA				
			ACTGTC	TTTTTTATTT				
			CTA					
GAM19	IFNA1	3'	GCTTCATGAATTCTGTCA	194	GAAAAA	A		
			TGACAGAA	AT	AAAGC			
			ACTGTCTT	TA	TTTCG			
			AAG	__	C			
GAM19	KCNJ6	5'	TTTTTTTTCTTGTCCA	60	A	T		
			TG	CAGAAGAAAAAA	AAAA			

AC GTCTTCTTTTTT TTTT
C T
GAM19 OTP 3' GCTTTTATTTTATTTATC 212 C GA
GA AGAA AAAAATAAAAGC
|| |||| |||||||
CT TTTT TTTTTATTTCG
A A_

GAM19 RHEB2 3' ATGCTTCTTTCTTGTAA 94 TAA
TGACAGAAGAAAAAA AAGCAT
||||||| |||||
ATTGTCTTCTTTTT TTTCGTA
C_

GAM19 ANKRD6 3' ATGCTTTATTCCCTTGTAA 137 AGAAAA
TGACAGA AATAAAAGCAT
||||| |||||||
ATTGTTT TTATTTTCGTA
CCC_

GAM19 EVI5 3' TGCAGGTTTCTTCTTCA 95 C ATAAAAA
TGA AGAAGAAAAA GCA
||| ||||| |||
ACT TCTTCTTTTT CGT
_ GGA_

GAM19 FLJ00026 3' ATGCTTGCTTTCTTATG 270 G TA_
TCA TGACA AAGAAAAAA AAAGCAT
|||| ||||| |||||
ACTGT TTCTTTTTT TTTCGTA
A TCG

GAM19 GP5 3' ATGCTCATATCATTCTTCTTCT 84 C _ AA
TCA TGA AGAAGAAAAA ATA AGCAT
||| ||||| ||| |||||
ACT TCTTCTTTTT TAT TCGTA
_ AC AC

GAM19 KHDRBS3 3' ATGCTAGTTTTCTTCTTCTT 107 C AAA
GA AGAAGAAAAAT AGCAT
||| ||||| |||||
TT TCTTTTTTTTG TCGTA
C A_

GAM19 KIAA0254 3' TGCTGTGTTCTTGTCA 132 _ AAAATAAA
TGACAGAA GAA AGCA
||| ||| |||||
ACTGTCTT CTT TCGT
T GTG_

GAM19 KIAA1165 3' ATGCTTTATAACCTCTGT 281 AAAAATA
ACAGAAGA AAAGCAT
||||| |||||||
TGTCTTCT TTTCGTA
CCAATA_

GAM19 KIAA1240 3' GTGGCCATTCTTGTCA 277 AAAA
TGACAGAAGAAAAAT GC
||||||| |||

		ACTGTCTTCTTTTTA	TG	
		CCGG		
GAM19	NYD-SP15	3' ATGCCATTTTTCTTCTGT	209	TAAAAA
		ACAGAAGAAAAAA	GCAT	
		TGTCTTCTTTTT	CGTA	
		TTAC_		
GAM19	PELI1	5' GCTTACTCTTCTTGTC	175	AAATA
		GACAGAAGAAA	AAAGC	
		CTGTCTTCTT	TTTCG	
		CTCA_		
GAM19	PRO0159	5' TTATTTTTCCCTGTCA	125	AA
		TGACAG GAAAAAATAA		
		ACTGTT CTTTTTATT		
		C_		
GAM19	RACGAP1	3' ATGTGAGCTTTCTTCTGTTA	121	ATAAAAA
		TGACAGAAGAAAAA	GCAT	
		ATTGTCTTCTTTT	TGTA	
		CGAG_		
GAM19	SDFR1	3' TTATCTTTCTTCTGTTA	118	A
		TGACAGAAGAAAAA ATAA		
		ATTGTCTTCTTT TATT		
		C		
GAM19	SDFR1	3' TTATCTTTCTTCTGTTA	151	A
		TGACAGAAGAAAAA ATAA		
		ATTGTCTTCTTT TATT		
		C		
GAM19	SS18L1	3' TTATTCTATCTTCTGTCA	272	AAA
		TGACAGAAGA AATAA		
		ACTGTCTTCT TTATT		
		ATC		
GAM19	SV2B	3' ATGTTTACTCTCCTCTGTCA	136	AAAAAAATAA
		TGACAGAAG AAGCAT		
		ACTGTCTTC TTTGTA		
		CTCTCA_		
GAM19	LOC130589	3' TGCTTTATTCCTCCTCCTTC	244	CA A AA
		A	TGA GA GA AAATAAAAGCA	
		ACT CT CT TTTATTTCGT		
		TC C CC		
GAM19	LOC200107	3' ATGCTTTACTTTCTTTT	364	A
		AGAAGAAAAA TAAAAGCAT		

TTTTCTTTTT ATTTCGTA
 C
 GAM19 LOC203340 3' TGCTTTTATTTCCCTC 368 AA
 GAAG AAAATAAAAGCA
 ||||| |||||
 CTTC TTTTATTTCGT
 C_

GAM19 LOC221271 3' TGCCTTTTTCTGTCA 380 ATAAAAA
 TGACAGAAGAAAAA GCA
 ||||| |||||
 ACTGTCTTTTTT CGT
 C_____

GAM19 LOC254778 3' ATGCTTTCTTCTATCA 400 C AAATAAA
 TGA AGAAGAAA AGCAT
 ||||| |||||
 ACT TCTTCTTT TCGTA
 A _____

GAM19 LOC51312 5' GCTTTTATTTCTCCTCT 164 A A
 AGA GA AAAATAAAAGC
 ||||| |||||
 TCT CT TTTTATTTCG
 C C

GAM19 LOC91286 5' TTTTTATTTCTTTCTGTCA 273 A
 TGACAGAAGAA AAATAAAAG
 |||||
 ACTGTCTTTTT TTTTTTTT
 C

GAM19 LOC92223 3' ATGCTTTATTGTACCTC 286 AAAAA
 GAAG AATAAAAGCAT
 ||||| |||||
 CTTC TTATTTCGTA
 CATG

GAM19 LOC92482 5' TGCACTTTCTTCTGT 288 A AAAAA
 ACAGAAGAAAA AT GCA
 ||||| || |||||
 TGTCTTCTTT TA CGT
 C _____

GAM20 ATRN 3' CTATCTGATGCACAGAA 248 G AAG
 TT TGTGCATCA GATAG
 ||||| |||||
 AA ACACGTAGT CTATC
 G _____

GAM20 ATRN 3' CTATCTGATGCACAGAA 248 G AAG
 TT TGTGCATCA GATAG
 || ||||| |||||
 AA ACACGTAGT CTATC
 G _____

GAM20 DKFZP564O0463 3' CTTTTCTTAATGCATACAATA 127 CAA T
 TATTGTGTGCAT AGGA AGAG
 ||||| ||||| |||||

	ATAACATACGTA	TTCT TTTC	
	A_ T		
GAM20	DKFZP564O0463 3'	CTTTTTCTTAATGCATACAATA 127	CAA T
	TATTGTGTGCAT	AGGA AGAG	
	ATAACATACGTA	TTCT TTTC	
	A_ T		
GAM20	FLJ13102 3'	CTCTACCCTCTCCCACCA 202	CATCAA_ A
	GTA	TATTGTGTG	AGG TAGAG
	ATGACACAC	TCC ATCTC	
	CACCCCTC	C	
GAM20	FLJ13102 3'	CTCTACCCTCTCCCACCA 202	CATCAA_ A
	GTA	TATTGTGTG	AGG TAGAG
	ATGACACAC	TCC ATCTC	
	CACCCCTC	C	
GAM20	HSPC014 3'	CTGTAATTTGATGTACACAA 144	GG
	TTGTGTGCATCAA	ATAG	
	AACACATGTAGTTT	TGTC	
	AA		
GAM20	HSPC014 3'	CTGTAATTTGATGTACACAA 144	GG
	TTGTGTGCATCAA	ATAG	
	AACACATGTAGTTT	TGTC	
	AA		
GAM20	KIAA0040 3'	TCTATCCCCCTGTCACATA 129	_ TCAA
	TGTGTG CA	GGATAGA	
	ATACAC GT	CCTATCT	
	T TCC	__	
GAM20	KIAA0040 3'	TCTATCCCCCTGTCACATA 129	_ TCAA
	TGTGTG CA	GGATAGA	
	ATACAC GT	CCTATCT	
	T TCC	__	
GAM20	KIAA0470 3'	CCACTTGATGCACAAATA 134	G A_
	TATT TGTGCATCAA	GG	
	ATAA ACACGTAGTT	CC	
	CA		
GAM20	KIAA0470 3'	CCACTTGATGCACAAATA 134	G A_
	TATT TGTGCATCAA	GG	
	ATAA ACACGTAGTT	CC	
	CA		
GAM20	KIAA1908 5'	CTCTCGGGCGATGCACACAA 302	AAAGGAT
	TTGTGTGCATC	AGAG	

	AACACACGTAG	TCTC	
	CGGGC_		
GAM20	KIAA1908 5' CTCTCGGGCGATGCACACAA	302	AAAGGAT
	TTGTGTGCATC	AGAG	
	AACACACGTAG	TCTC	
	CGGGC_		
GAM20	MGC22014 3' CTCTATCCTTGTATATCACAA	269	TGCATCA
	A	TATTGTG AAGGATAGAG	
	ATAACAC TTCCTATCTC		
	TATATG_		
GAM20	MGC22014 3' CTCTATCCTTGTATATCACAA	269	TGCATCA
	A	TATTGTG AAGGATAGAG	
	ATAACAC TTCCTATCTC		
	TATATG_		
GAM20	TNRC9 3' CTGTATTTGATGCAACAA	293	G G
	TTGT TGCATCAAAG ATAG		
	AACA ACGTAGTTT TGTC		
	— A		
GAM20	TNRC9 3' CTGTATTTGATGCAACAA	293	G G
	TTGT TGCATCAAAG ATAG		
	AACA ACGTAGTTT TGTC		
	— A		
GAM20	LOC116123 3' CTTTGGTTTGATGCATACAATA	243	GGA
	TATTGTGTGCATCAAA TAGAG		
	ATAACATACGTAGTTT GTTTC		
	G_		
GAM20	LOC116123 3' CTTTGGTTTGATGCATACAATA	243	GGA
	TATTGTGTGCATCAAA TAGAG		
	ATAACATACGTAGTTT GTTTC		
	G_		
GAM20	LOC149721 3' CTATCATGTGGATGCACACA	334	AAAG_
	TGTGTGCATC GATAG		
	ACACACGTAG CTATC		
	GTGTA		
GAM20	LOC149721 3' CTATCATGTGGATGCACACA	334	AAAG_
	TGTGTGCATC GATAG		
	ACACACGTAG CTATC		
	GTGTA		
GAM20	LOC153338 5' CTCTATCCCTCTGTGGCCAATA	354	T G CAAA
	TATTG GT CAT GGATAGAG		

		ATAAC CG GTG CCTATCTC _ _ TCTC			
GAM20	LOC153338 5'	CTCTATCCCTCTGTGGCCAATA 354	T G	CAA	
		TATTG GT CAT GGATAGAG 			
		ATAAC CG GTG CCTATCTC _ _ TCTC			
GAM20	LOC220766 3'	CCACTTGATGCACAAATA 375	G	A_	
		TATT TGTGCATCAA GG 			
		ATAA ACACGTAGTT CC _ CA			
GAM20	LOC220766 3'	CCACTTGATGCACAAATA 375	G	A_	
		TATT TGTGCATCAA GG 			
		ATAA ACACGTAGTT CC _ CA			
GAM20	LOC253351 5'	CTGGCACCTGATGCACACAA 402		AAGGA	
		TTGTGTGCATCA TAG 			
		AACACACGTAGT GTC CCACG			
GAM20	LOC253351 5'	CTGGCACCTGATGCACACAA 402		AAGGA	
		TTGTGTGCATCA TAG 			
		AACACACGTAGT GTC CCACG			
GAM20	LOC257484 3'	CTCTATCCTGTATATCACAAT 366		TGCATCA	
	A	TATTGTG AAGGATAGAG 			
		ATAACAC TTCCTATCTC TATATG_			
GAM20	LOC257484 3'	CTCTATCCTGTATATCACAAT 366		TGCATCA	
	A	TATTGTG AAGGATAGAG 			
		ATAACAC TTCCTATCTC TATATG_			
GAM21	KIAA1843 3'	ATAGAAAGTAGCCAAAAAA 267	CTG		
		TTTTTG TACTTTCTAT 			
		AAAAAAC ATGAAAGATA CG_			
GAM21	SDFR1 3'	AAAGTACAGCAAAACCTA 117	T		
		TAG TTTTGCTGTACTTT 			
		ATC AAAACGACATGAAA C			
GAM21	SDFR1 3'	AAAGTACAGCAAAACCTA 150	T		
		TAG TTTTGCTGTACTTT 			

		ATC AAAACGACATGAAA	
		C	
GAM21	LOC132617 3'	CTACAGACCATAGCAAAAAC	314
		GTTTTGCTGT	TCT TAG
		CAAAAACGATA	AGA ATC
		CC_ C	
GAM21	LOC145622 3'	CTATAGAACAAATGCAAAAAC	322
		GTTTTGC	TTCTATAG
		CAAAAACG	AAGATATC
		TAAC_	
GAM21	LOC222681 3'	CTACAGAACATGGAGCAAAAAC	386
	TA	TAGTTTTGCT TA	TTCT TAG
		ATCAAAAACGA GT	AAGA ATC
		G AC C	
GAM21	LOC257507 3'	CTACAGAACATGGAGCAAAAAC	405
	TA	TAGTTTTGCT TA	TTCT TAG
		ATCAAAAACGA GT	AAGA ATC
		G AC C	
GAM21	LOC257625 3'	CTACAGAACATGGAGCAAAAAC	406
	TA	TAGTTTTGCT TA	TTCT TAG
		ATCAAAAACGA GT	AAGA ATC
		G AC C	
GAM22	BTEB1	3' ACCACTACATCCATCT	53
		GCA	
		AGATGGGTG	AGTGGT
		TCTACCTAC	TCACCA
		A_	
GAM22	CEP2	3' ACCACCTCCTTCATCTT	112
		T CAA	
		AAGATGGG GG	GTGGT
		TTCTACTT CC	CACCA
		_ TC_	
GAM22	ECM1	3' ACCCTGCCCAACCATCT	82
		CA_ T	
		AGATGGGTGG	AG GGT
		TCTACCCACC	TC CCA
		CCG _	
GAM22	ENG	3' ACCACTTGCCACGCTGTT	34
		_	
		GATGG GTGGCAAGTGGT	
		TTGTC CACCGTTACCA	
		G	
GAM22	ESRRG	3' ACCACTTTCAGCCATT	276
		G C	
		AGATGG TGG AAGTGGT	

TTTACCA ACT TTCACCA
G T
GAM22 HDAC4 3' ACCACTCGACTCATCTTG 98 GGCA
TAAGATGGGT AGTGGT
||||||| |||||
GTTCTACTCA TCACCA
GC__

GAM22 IL6 3' ACCACTTGAAACATTATA 41 GGTGG
TAAGATG CAAGTGGT
||||| |||||
ATTTTAC GTTCACCA
AAA__

GAM22 LRAT 3' ACCACTAAAATTATCTTA 259 GTGGC
TAAGATGG AAGTGGT
||||||| |||||
ATTCTATT TTCACCA
AAAA__

GAM22 MYLK2 3' ACCACTCGGGGCCCCATCTTG 226 T A__
TAAGATGGG GGC AGTGGT
||||||| |||||
GTTCTACCC CCG TCACCA
_ GGGC

GAM22 PRKACB 3' ACCACTTCTTTCATCT 61 T C
AGATGGG GG AAGTGGT
||||| |||||
TCTACTT TC TTCACCA
T __

GAM22 PRLR 3' ACCACTTGCCTCTTCT 51 T T
AGA GGG GGCAAGTGGT
||| ||| |||||
TCT TCT CCGTTCACCA
T __

GAM22 SLC6A6 3' ACCACTTGAATTGATCTT 65 G GG
AAGAT GGT CAAGTGGT
||||||| |||||
TTCTA TTA GTTCACCA
G A__

GAM22 WASF3 3' ACCACTTGGTCAGAATTATA 109 GGG __
TAAGAT TGGC AAGTGGT
||||| |||||
ATTTTA ACTG TTCACCA
AG__ G

GAM22 XK 3' ACCACTTGCACTATTCTTA 181 TG G
TAAGA GGTG CAAGTGGT
||||| |||||
ATTCT TCAC GTTCACCA
TA __

GAM22 ZYX 3' ACCACCTGCCACCT 69 A T A
AG TGGG GGCA GTGGT
|| ||||| |||||

TC ACCC CCGT CACCA
 C _ C
 GAM22 ARHF 3' ACCCTGGACCACCCATCT 167 CA_ T
 AGATGGGTGG AG GGT
 ||||| |||||
 TCTACCCACC TC CCA
 AGG _
 GAM22 DDR1 5' CGCACCACCCATTAA 57 CAA
 TAAGATGGGTGG GTG
 |||||||| |||||
 ATTTACCCACC CGC
 A__
 GAM22 DDR1 5' CGCACCACCCATTAA 122 CAA
 TAAGATGGGTGG GTG
 |||||||| |||||
 ATTTACCCACC CGC
 A__
 GAM22 DDR1 5' CGCACCACCCATTAA 123 CAA
 TAAGATGGGTGG GTG
 |||||||| |||||
 ATTTACCCACC CGC
 A__
 GAM22 DKFZP547E1010 5' ACCACCTCCCTATCTTA 141 TG CAA
 TAAGATGGG G GTGGT
 ||||||| | |||||
 ATTCTATCC C CACCA
 CT __
 GAM22 DKFZP547E1010 5' ACCACCTCCCTATCTTA 280 TG CAA
 TAAGATGGG G GTGGT
 ||||||| | |||||
 ATTCTATCC C CACCA
 CT __
 GAM22 FLJ11715 3' ACCCGGCCAGCCCCATCT 197 __ AA
 AGATGGT GGC GTGGT
 ||||||| |||||
 TCTACCCG CCG CGCCA
 AC __
 GAM22 FLJ12587 3' ACCAGGGCCCGATCCATCT 190 __ AAG
 AGATGG GTGGC TGTT
 ||||| ||||| |||||
 TCTACC CGCCG ACCA
 TA GG__
 GAM22 FLJ12650 3' ACCACTTGCCAATGCCTCTC 196 T __
 GA GGGT GGCAAGTGGT
 || |||| |||||||||
 CT TCCG CCGTTCACCA
 C TAA
 GAM22 FLJ13265 3' ACCACTTGCCCTGCCTCA 201 - __
 TG GGT GGCAAGTGGT
 || |||| |||||||||

AC CCG CCGTTCACCA
T TC
GAM22 FLJ20546 3' ACCTCTGCCACCCATCT 155 AT
AGATGGGTGGCA G GGT
||||||| |||||
TCTACCCACCGT C CCA
_ T
GAM22 FLJ32865 3' ACCACCACGCCAGCTTA 251 A GCAA
TAAG TGGGTG GTGGT
||||||| |||||
ATTC ACCCGC CACCA
G AC__
GAM22 GPR88 3' ACCACTTGTTGTACATCT 185 G TG
AGATG G GCAAGTGGT
||||| | |||||||
TCTAC T TGTTCACCA
A GT
GAM22 HSPC216 3' ACCTGACCACCCATT 149 _ AGT
AGATGGGTGG CA GGT
||||||| || |||
TTTACCCACC GT CCA
A __
GAM22 JIK 3' ACCACATTCCCCATTAA 148 T CAA
TAAGATGGG GG GTGGT
||||||| || |||||
ATTTACCC CT CACCA
_ TA__
GAM22 KIAA0153 3' ACCACCCAGCAAGCCCCCTTA 139 A G_ AA__
TAAG TGGGT GC GTGGT
||||||| || |||||
ATTC GCCCG CG CACCA
C AA ACC
GAM22 KIAA0215 3' ACCAGGAGACCACCATCTTA 130 G CAAG__
TAAGATGG TGG TGTT
||||||| || |||||
ATTCTACC ACC ACCA
_ AGAGG
GAM22 KIAA0461 3' ACCACTTGTTGAAATCCA 291 __
TGGGT GGCAAGTGGT
||||| |||||||
ACCTA TTGTTCACCA
AAG
GAM22 MEGF10 3' ACCACAGACTCATCTTA 216 GGCAA
TAAGATGGGT GTGGT
||||||| |||||
ATTCTACTCA CACCA
GA__
GAM22 MGC2452 5' ACCACTAATTGCCACTCA 218 __
TGGGTGGCA AGTGGT
||||||| |||||

ACTCACCGT TCACCA
TAA
GAM22 MGC4796 3' ACCTTCACCTCATCTTA 266 _ CAAGT
TAAGATG GGTGG GGT
|||||| |||| |||
ATTCTAC CCACT CCA
T T_

GAM22 MRPL10 3' ACCACATTGTACCCATTT 256 G _
AGATGGGTG CAA GTGGT
|||||| |||| |||||
TTTACCCAT GTT CACCA
_ A

GAM22 MRPL42 5' ACCACTTGATAAGCATCTTG 299 GG G
TAAGATG TG CAAGTGGT
|||||| || |||||
GTTCTAC AT GTTCACCA
GA A

GAM22 POLYDOM 3' ACCACTGCTATCCATCTT 195 A
AAGATGGGTGGCA GTGGT
|||||||||| |||||
TTCTACCTATCGT CACCA

GAM22 PRO0246 5' ACCACTTGCTATGGTCT 126 GG
AGAT GTGGCAAGTGGT
||| |||||||||
TCTG TATCGTTACCA
G_

GAM22 SMCR7 3' ATGACTTGCCACCCACCT 247 A G
AG TGGGTGGCAAGT GT
|| ||||||||| ||
TC ACCCACC GTTCA TA
C G

GAM22 TPD52 3' ACCACTTATATCAACTTA 88 ATG GC
TAAG GGTG AAGTGGT
|||| |||| |||||
ATTC CTAT TTCACCA
AA_ A_

GAM22 ZNF384 3' ACCACTCATCACGGCCATCTT 239 _ CA
AAGATGG GTGG AGTGGT
|||||| |||||
TTCTACC CACT TCACCA
GG AC

GAM22 LOC124216 3' ACCTCTCCTCACCCATCTTA 307 CA T
TAAGATGGGTGG AG GGT
|||||| || |||
ATTCTACCCACT TC CCA
CC T

GAM22 LOC144509 5' ACCACCAGCTGCACCCATCT 320 _ AA
AGATGGGTG GC GTGGT
|||||| || |||||

TCTACCCAC CG CACCA
GT AC

GAM22 LOC146822 3' ACCACCTGCCCTACCATT 324 GT_ A
AGATGG GGCA GTGGT
|||||| |||||
TTTACC CCGT CACCA
ATC C

GAM22 LOC148371 5' ACCACTCTGGCCATCT 330 G C
AGATGG TGG AAGTGGT
|||||| |||||
TCTACC GTC TTCACCA
G _

GAM22 LOC149373 3' ACCTGCCGGCCACCCATTCA 333 A AA _
A GATGGGTGGC GT GGT
| ||||| || |||
A TTACCCACCG CG CCA
C GC T

GAM22 LOC151146 5' ACCCCCCAGCCCATCTTA 336 _ CAAGT
TAAGATGGG TGG GGT
||||||| || |||
ATTCTACCC ACC CCA
G CC __

GAM22 LOC157562 5' ACCACCCAGTCATTTA 357 G CAA
TAAGATGG TGG GTGGT
||||||| || |||||
ATTTTACT ACC CACCA
G __

GAM22 LOC160897 3' ACCACTTATAATGCCTCATCTT 341 _ GC __
A TAAGATG GGTG AAGTGGT
||||||| || |||||
ATTCTAC CCGT TTCACCA
T AATA

GAM22 LOC161589 5' ACCACTGCTGCCATCT 343 G A
AGATGG TGGCA GTGGT
||||||| || |||||
TCTACC GTCGT CACCA
G __

GAM22 LOC163682 5' ACCACTTGGCGAGCTCCTA 361 ____
TGGG TGGCAAGTGGT
||| ||||| |||||
ATCC GCCGTTCACCA
TCGA

GAM22 LOC199692 3' ACCAGTAACCTATCTTA 257 G AAG
TAAGATGGGT GC TGTT
||||||| || |||||
ATTCTATCCA TG ACCA
A __

GAM22 LOC202108 5' ACCACTACTGGCCATCT 367 G CA
AGATGG TGG AGTGGT
||||||| || |||||

TCTACC GTC TCACCA
G A_
GAM22 LOC221468 3' ACCACCCCAGTTCTTCATCTT 258 TG AA_
AAGATGGG GC GTGGT
|||||| || ||||
TTCTACTT TG CACCA
CT ACC
GAM22 LOC221838 5' ACCACTACTGGCCATCT 385 G CA
AGATGG TGG AGTGGT
|||||| |||||
TCTACC GTC TCACCA
G A_
GAM22 LOC221839 5' ACCACTACTGGCCATCT 384 G CA
AGATGG TGG AGTGGT
|||||| |||||
TCTACC GTC TCACCA
G A_
GAM22 LOC90313 5' ACCACCCCCTGTGCCCATC 268 G A_
GATGGGTG CA GTGGT
|||||| || ||||
CTACCCGT GT CACCA
_ CCC
GAM22 LOC92399 3' ACCACCTGCTCCTCATCTTA 242 TG A
TAAGATGGG GCA GTGGT
|||||| |||||
ATTCTACTC CGT CACCA
CT C
GAM23 ADAM8 3' AGAGAAGCCATGCGTTCC 52 A T CAA
C GAC CAT GCTTCTCT
| |||| |||||
C TTG GTA CGAAGAGA
C C C_
GAM23 BN51T 3' AGAGAGCAAGGATTGAGTCTG 363 _ AA_ T
CAGACTCA TC GCT CTCT
|||||| || |||||
GTCTGAGT AG CGA GAGA
T GAA _
GAM23 CD3Z 3' AGACTGACCTTGATGAGCTG 48 A C C_
CAG CTCATCAAG TT TCT
|||||| || |||||
GTC GAGTAGTTC AG AGA
_ C TC
GAM23 DAAM2 3' AGGTGCTTGATGAATCTG 381 C T
CAGA TCATCAAGC TCT
|||||| |||||
GTCT AGTAGTTCG GGA
A T
GAM23 DLG4 3' AGGGAGGGATGGGTCT 54 AAG
AGACTCATC CTTCTCT
|||||| |||||

TCTGGGTAG GGAGGGA

GAM23	DMD	5' AGAAAAGCTTGAGCAAGTC	73	CA_	C
		GACT	TCAAGCTT TCT		
		CTGA	AGTCGAA AGA		
		ACG	A		
GAM23	DMD	5' AGAAAAGCTTGAGCAAGTC	74	CA_	C
		GACT	TCAAGCTT TCT		
		CTGA	AGTCGAA AGA		
		ACG	A		
GAM23	DMD	5' AGAAAAGCTTGAGCAAGTC	75	CA_	C
		GACT	TCAAGCTT TCT		
		CTGA	AGTCGAA AGA		
		ACG	A		
GAM23	E2F1	3' AGGCCTCTTGGTGAGCCTG	348	A	—
		CAG CTCATCAA	GCTT		
		GTC GAGTGGTT	CGGA		
		C	TCTC		
GAM23	EBP	3' AGAGAACGCCAGGAGGTCT	108	CA AA_	
		AGACT TC	GCTTCTCT		
		TCTGG AG	CGAAGAGA		
		— GAC			
GAM23	FANCG	5' AGAGAACGCCAGGGAGCTC	85	_ A AA	
		GA CTC TC	GCTTCTCT		
		CT GAG GG	CGAAGAGA		
		C _ GA			
GAM23	FE65L2	5' AGGCGCCTGATGAGTTCA	99	A	A T
		C GACTCATCA	GC TCT		
		A TTGAGTAGT	CG GGA		
		C C C			
GAM23	FE65L2	5' AGGCGCCTGATGAGTTCA	236	A	A T
		C GACTCATCA	GC TCT		
		A TTGAGTAGT	CG GGA		
		C C C			
GAM23	FE65L2	5' AGGCGCCTGATGAGTTCA	237	A	A T
		C GACTCATCA	GC TCT		
		A TTGAGTAGT	CG GGA		
		C C C			
GAM23	FE65L2	5' AGGCGCCTGATGAGTTCA	238	A	A T
		C GACTCATCA	GC TCT		

			A TTGAGTAGT CG GGA		
			C C C		
GAM23	FGFR4	3'	AGAGAAGCTGGAAGCCTG	193	A CA A
			CAG CT TC AGCTTCTCT		
			GTC GA AG TCGAAGAGA		
			C __ G		
GAM23	FGFR4	3'	AGAGAAGCTGGAAGCCTG	58	A CA A
			CAG CT TC AGCTTCTCT		
			GTC GA AG TCGAAGAGA		
			C __ G		
GAM23	FHL1	3'	AGAGAAGCTGATGCCTC	55	CT A
			GA CATCA GCTTCTCT		
			CT GTAGT CGAAGAGA		
			CC _		
GAM23	GCNT2	5'	AGAGAACGAGTGAGTTG	56	CAAGC
			CAGACTCAT TTCTCT		
			GTTTGAGTG AAGAGA		
			AGCA_		
GAM23	GNRHR	5'	AGAGAAGCTGGTAATTCTG	38	CTC A
			CAGA ATCA GCTTCTCT		
			GTCT TGGT CGAAGAGA		
			TAA _		
GAM23	HIS1	5'	AGGGGAGATGAGTTG	105	AAG
			CAGACTCATC CTTCT		
			GTTTGAGTAG GGGGA		
			A_		
GAM23	HNRPDL	3'	AGAAAGGTATGAGTTG	92	CAA C
			CAGACTCAT GCTT TCT		
			GTTTGAGTA TGGA AGA		
			A		
GAM23	INHBA	3'	AGAAAGCCATGAGTTG	59	CAA C
			CAGACTCAT GCTT TCT		
			GTTTGAGTA CGAA AGA		
			C__ _		
GAM23	KIF3B	3'	AGAGAAGCTCATAGTGTG	87	G C CA
			CA ACT AT AGCTTCTCT		
			GT TGA TA TCGAAGAGA		
			G A C_		
GAM23	MSN	3'	AGAGAAGCCTGTGCCCTG	262	ACT T A
			CAG CA CA GCTTCTCT		

		GTC	GT	GT	CGAAGAGA			
		CC	_	C				
GAM23	MTR	3'	AGAGAAAGTGTGACCCCTG	36	AC	CAA		
		CAG	TCAT	GCTTCTCT				
		GTC	AGTG	TGAAGAGA				
		CC	__					
GAM23	PCDHB9	3'	AGAGAAAGTTAGATCCTG	169	ACTC	A		
		CAG	ATC	AGCTTCTCT				
		GTC	TAG	TTGAAGAGA				
		C	__	A				
GAM23	SMARCA3	3'	AGAGAAGCTTCATGTTG	246	TCATC			
		CAGAC	AAGCTTCTCT					
		GTTTG	TTCGAAGAGA					
		TAC	__					
GAM23	SMARCA3	3'	AGAGAAGCTTCATGTTG	66	TCATC			
		CAGAC	AAGCTTCTCT					
		GTTTG	TTCGAAGAGA					
		TAC	__					
GAM23	SMG1	3'	AGACAGTAGATGAGTCTG	138	AA	_		
		CAGACTCATC	GCT TCT					
		GTCTGAGTAG	TGA AGA					
		A	__	C				
GAM23	SNCAIP	5'	AGAAAGGGGGTGAGTCTG	399	AAG	C		
		CAGACTCATC	CTT TCT					
		GTCTGAGTGG	GAA AGA					
		GG	__					
GAM23	SYNGR1	3'	AGGGGAGCGATGAGCTG	86	A	AA		
		CAG	CTCATC	GCTTCTCT				
		GTC	GAGTAG	CGAGGGGA				
		—	—	—				
GAM23	UCP2	5'	AGAGAAGCTTGATCTGGAG	68	—	—		
		CTC	ATCAAGCTTCTCT					
		GAG	TAGTCGAAGAGA					
		GTTC						
GAM23	BMF	3'	AGAGGCTGATGTGCTG	229	T	A		
		CAGAC	CATCA	GCTTCT				
		GTCTG	GTAGT CGGAGA					
		T	—					
GAM23	BNIP2	3'	AGAGAATGTGATGAGTT	278	AGC			
		GA	CTCATCA	TTCTCT				

TTGAGTAGT AAGAGA
GT_

GAM23 DDX33 3' AGAGAACGCCTTCCAATC 171 C AT _
GA TC CAAG CTTCTCT
|| || |||||
CT AG GTTC GAAGAGA
A _ C

GAM23 EML4 3' AGAAAACTTGGATGAGTT 168 _ C
GACTCATC AAG TTCT
||||||| |||||
TTGAGTAG TTC AAGA
GT A

GAM23 EPB41L4 3' AGAGAACGAAATGGGTCT 187 CAAG
AGACTCAT CTTCTCT
||||||| |||||
TCTGGGTA GAAGAGA
AA_

GAM23 FLJ11588 5' AGAGAACGCAGAACGCCCTG 199 A CA AA
CAG CT TC GCTTCTCT
||| || || |||||
GTC GG AG CGAACAGA
C CA A_

GAM23 FLJ20150 3' AGAGAACGCCTGTGGCT 153 A T T A
AG C CA CA GCTTCTCT
||| || || |||||
TC G GT GT CGAACAGA
-- _ C

GAM23 FLJ20507 3' AGATGTTGATGAGGCTG 154 A G T
CAG CTCATCAA C TCT
||| ||||| | |||
GTC GAGTAGTT G AGA
G _ T

GAM23 FLJ20507 3' AGATGTTGATGAGGCTG 261 A G T
CAG CTCATCAA C TCT
||| ||||| | |||
GTC GAGTAGTT G AGA
G _ T

GAM23 FLJ20972 3' AGAGAACGCAGTTGGCATCTG 205 C_ TCAA
CAGA TCA GCTTCTCT
||| || |||||
GTCT GGT CGAACAGA
AC TGA_

GAM23 FLJ22233 3' AGAGAACGCTAGAACGTC 204 CA A
GACT TC AGCTTCTCT
||| || |||||
CTGA AG TCGAACAGA
— A

GAM23 FLJ23191 3' AGAGAACGTTGTGACCTG 198 AC CA
CAG TCAT AGCTTCTCT
||| || |||||

GTC AGTG TTGAAGAGA
 C_ _
 GAM23 FLJ23468 5' AGAGAAACCAGCTGAGTCTG 200 TCAA _
 CAGACTCA GCT TCTCT
 ||||| |||||
 GTCTGAGT CGA AGAGA
 _____ CCAA
 GAM23 GIT2 3' AGAGAACATCAGTCT 133 C CAA
 AGACT AT GCTTCTCT
 ||||| |||||
 TCTGA TA CGAAGAGA
 C _
 GAM23 GIT2 3' AGAGAACATCAGTCT 231 C CAA
 AGACT AT GCTTCTCT
 ||||| |||||
 TCTGA TA CGAAGAGA
 C _
 GAM23 GIT2 3' AGAGAACATCAGTCT 232 C CAA
 AGACT AT GCTTCTCT
 ||||| |||||
 TCTGA TA CGAAGAGA
 C _
 GAM23 GRID1 3' AGAGAACCTAGGTGGGCT 285 A AA_
 AG CTCATC GCTTCTCT
 ||||| |||||
 TC GGGTGG CGAAGAGA
 _ ATC
 GAM23 GT650 3' AAGCTTCTATGAGTTG 230 C_
 CAGACTCAT AAGCTT
 ||||| |||||
 GTTGAGTA TTCGAA
 TCT
 GAM23 IKKE 3' AGGACTGTGAGTCTG 124 CA C
 CAGACTCAT AG TTCT
 ||||| |||||
 GTCTGAGTG TC AGGA
 _ _
 GAM23 KIAA0254 5' AGAGGACCGCGATGAGTC 131 AA _
 GACTCATC GC TTCTCT
 ||||| |||||
 CTGAGTAG CG AGGAGA
 _ CC
 GAM23 KIAA1026 3' AGAGAACCTGCCTCAGTCTG 292 CATCA
 CAGACT AGCTTCTCT
 ||||| |||||
 GTCTGA TCGAAGAGA
 CTCCG
 GAM23 KIAA1163 3' AGAGAACATGTCTGAGTT 331 T_ A
 GACTCA CA GCTTCTCT
 ||||| |||||

TTGAGT GT CGAAGAGA
 CT A
 GAM23 KIAA1598 3' AGAACGCTCTGTTGGTCTG 161 TC_____
 CAGACTCA AAGCTTCT
 ||||| |||||
 GTCTGGGT TTCGAAGA
 TTTGTC

GAM23 KIAA1853 3' AGAACGCAATGGTCTG 287 CAA
 CAGACTCAT GCTTCT
 ||||| |||||
 GTCTGGTA CGAAGA
 A_____

GAM23 LOXL4 3' AGAGAACGCTGGTGGATC 213 CT A
 GA CATCA GCTTCTCT
 || |||||
 CT GTGGT CGAAGAGA
 AG _____

GAM23 METAP1 3' AGAGAACGCGTGAAGTTG 298 CA A
 CAGACT TCA GCTTCTCT
 ||||| |||||
 GTTGAGT CGAAGAGA
 _____ G

GAM23 MGC11034 3' AGAGAACGCTCTTGAAGTT 211 _ TCA
 GACT CA AGCTTCTCT
 ||||| |||||
 TTGA GT TCGAAGAGA
 A TTC

GAM23 MGC14128 3' AGAACGCTTGAGAGCCTG 222 A A _____
 CAG CTC TCAA GCTTCT
 ||||| |||||
 GTC GAG AGTT CGAAGA
 C _____ T

GAM23 MGC16175 5' AGAGGCTGTGAGTCTG 219 CA
 CAGACTCAT AGCTTCT
 ||||| |||||
 GTCTGAGTG TCGGAGA

GAM23 MGC2752 5' AGAGAACGCTCAGTAGAATC 327 C _ CA
 GA TC AT AGCTTCTCT
 ||||| |||||
 CT AG TG TCGAAGAGA
 A A AC

GAM23 MGC34923 3' AGAGAACGTTAGGAAGAGCCTG 254 A A AA
 CAG CTC TC GCTTCTCT
 ||||| |||||
 GTC GAG AG TGAAGAGA
 C A GA

GAM23 NR1I3 5' AGAGAACGAGGAGTCTG 89 ATCAA
 CAGACTC GCTTCTCT
 ||||| |||||

		GTCTGAG	CGAAGAGA	
		GA	_____	
GAM23	NYD-SP15	3' AGAGAAGAAATATTGAGTCTG	208	TCAAG_____
		CAGACTCA	CTTCTCT	
		GTCTGAGT	GAAGAGA	
		TTATAAA		
GAM23	OSBPL8	5' AGAGAAGTTGGGGTCTG	177	ATCAA
		CAGACTC	GCTTCTCT	
		GTCTGGG	TGAAGAGA	
		GT	_____	
GAM23	PLEKHA4	5' AGAGACCCCTGTGAGTCTG	178	CA CT
		CAGACTCAT	AG TCTCT	
		GTCTGAGTG	TC AGAGA	
		__ CC		
GAM23	PRKWNK2	3' AGAGATGATTGAGTCTG	372	_ AGCT
		CAGACTCA	TCA TCTCT	
		GTCTGAGT	AGT AGAGA	
		T	_____	
GAM23	PSMD4	3' AGGGTAGCTGAGTCTG	63	TCAA T
		CAGACTCA	GCT CTCT	
		GTCTGAGT	CGA GGGAA	
		__ T		
GAM23	RIS1	3' AGAGAACGCTTTGTATCTG	337	CT TCA
		CAGA CA AGCTTCTCT		
		GTCT GT TCGAAGAGA		
		AT TTC		
GAM23	RNF24	3' AGAGGAGTGGATGAGCCTG	114	A AA
		CAG CTCATC	GCTTCTCT	
		GTC GAGTAG	TGAGGGAGA	
		C G	_____	
GAM23	SNURF	3' AGAAAAGCGGGTTTGGGTCTG	96	TCAA_ C
		CAGACTCA	GCTT TCT	
		GTCTGGGT	CGAA AGA	
		TTTGGG	A	
GAM23	SULT4A1	3' AGAGAACGCTTGTTTTG	284	CT T
		CAGA CA CAAGCTTCTCT		
		GTTT GT GTTCGAAGAGA		
		TT	_____	
GAM23	SV2B	3' AGAGAATTGTGTGAGTCTG	135	_ GC
		CAGACTCAT	CAA TTCTCT	

GTCTGAGTG GTT AAGAGA
T _
GAM23 SZF1 5' AGAGAACGCCTAGATATCTG 147 CTC AA_
CAGA ATC GCTTCTCT
||| ||| |||||
GTCT TAG CGAAGAGA
A_ ATC
GAM23 TLR10 5' AGAGAGGGTATTGAGTCTG 210 TCAAG
CAGACTCA CTTCTCT
|||||| |||||
GTCTGAGT GGAGAGA
TATG_
GAM23 ZNF185 3' AGAGGAGCTTGTGAATC 111 C T
GA TCA CAAGCTTCTCT
|| ||| |||||
CT AGT GTTCGAGGAGA
A _
GAM23 LOC113612 3' AGAAGGATGAGTTG 300 AAG
CAGACTCATC CTTCT
|||||| |||||
GTTGAGTAG GAAGA

GAM23 LOC133539 3' AGAGAACGCCAGGATGGTC 312 T AA_
GAC CATC GCTTCTCT
||| ||| |||||
CTG GTAG CGAAGAGA
— GACC

GAM23 LOC139221 5' AGAGAACACATGACCTG 313 AC CAA
CAG TCAT GCTTCTCT
||| ||| |||||
GTC AGTA CGAAGAGA
C_ CA_

GAM23 LOC142941 3' AAGTTTATTGTAATGAGTCTG 345 — —
CAGACTCAT CAA GCTT
|||||| ||| |||||
GTCTGAGTA GTT TGAA
AT ATT

GAM23 LOC145717 5' AGAGAGTGGGGGTGAGTCTG 279 AA_ T
CAGACTCATC GCT CTCT
|||||| ||| |||||
GTCTGAGTGG TGA GAGA
GGG _

GAM23 LOC147229 3' AGAGAACGCTGGCAAGAGCTG 325 A ATCA_
CAG CTC AGCTTCTCT
||| ||| |||||
GTC GAG TCGAAGAGA
— AACGG

GAM23 LOC147658 3' AGAAAAGTTGAAGTC 326 CA C
GACT TCAAGCTT TCT
||| ||||| |||||

CTGA AGTTGAA AGA
 — A
 GAM23 LOC147920 3' AGAGAAGCCTGAGGAATT 328 C A A
 AGA TC TCA GCTTCTCT
 ||| ||| |||||
 TTT AG AGT CGAAGAGA
 A G C

GAM23 LOC148894 5' AGAGAAGCTCCGTGGCCTG 347 A CA
 CAG CTCAT AGCTTCTCT
 ||| ||||| |||||
 GTC GGGTG TCGAAGAGA
 C CC

GAM23 LOC150606 3' AGAGAAGCTGGGTGATCTG 349 C A
 CAGA TCATC AGCTTCTCT
 ||| ||||| |||||
 GTCT AGTGG TCGAAGAGA
 — G

GAM23 LOC150606 3' AGAGAAGCTTGTGGTC 350 T T
 GAC CA CAAGCTTCTCT
 ||| ||| |||||
 CTG GT GTTCGAAGAGA

— —
 GAM23 LOC152220 3' AGAGTATTCTTGATGAATT 351 C CTT__
 AGA TCATCAAG CTCT
 ||| ||||| |||||
 TTT AGTAGTTC GAGA
 A TTTAT

GAM23 LOC155382 3' AGAGAAGCTGCAGGAGCTG 356 A ATCA
 CAG CTC AGCTTCTCT
 ||| ||| |||||
 GTC GAG TCGAAGAGA
 — GACG

GAM23 LOC157621 3' AGAGGGCGAAATGAGTCT 358 CAA T
 AGACTCAT GCT CTCT
 ||||| ||| |||||
 TCTGAGTA CGG GAGA
 AAG —

GAM23 LOC161528 5' AGAGAGTGGGGGTGAGTCTG 342 AA_ T
 CAGACTCATC GCT CTCT
 ||||| ||| |||||
 GTCTGAGTGG TGA GAGA
 GGG —

GAM23 LOC197114 5' AGAGAAGCCCGAGGGGGCTG 369 A A AA
 CAG CTC TC GCTTCTCT
 ||| ||| ||| |||||
 GTC GGG AG CGAAGAGA
 G G CC

GAM23 LOC199883 3' AGAAAGGCGGTGAGTC 370 AA C
 GACTCATC GCTT TCT
 ||||| ||| |||||

	CTGAGTGG CGGA AGA	
	— A	
GAM23	LOC200020 3' AGAAAGGCCGGTGAGTC 371	AA C
	GACTCATC GCTT TCT	
	CTGAGTGG CGGA AGA	
	— A	
GAM23	LOC200226 3' AGAGAAGCTCGTGAATGTT 365	— CA
	GAC TCAT AGCTTCTCT	
	TTG AGTG TCGAAGAGA	
	TA C_	
GAM23	LOC204820 5' AGAGAAGCCAGGCCAGCTG 373	A CA AA
	CAG CT TC GCTTCTCT	
	GTC GA GG CGAAGAGA	
	— CC AC	
GAM23	LOC219392 5' AGAGAAATCCTAGATGAGTC 377	A C_
	GACTCATC AG TTCTCT	
	CTGAGTAG TC AAGAGA	
	A CTA	
GAM23	LOC219800 3' AGAGAAGCTTGGGAGCCT 389	A A
	AG CTC TCAAGCTTCTCT	
	TC GAG GGTCGAAGAGA	
	C _	
GAM23	LOC220753 5' AGAGAAGCCAGAGGTGTG 388	G CA AA
	CA ACT TC GCTTCTCT	
	GT TGG AG CGAAGAGA	
	G _ AC	
GAM23	LOC220776 3' AGAGGGGTGATGATAAACTG 283	AC_ AA
	CAG TCATC GCTTCTCT	
	GTC AGTAG TGGGGAGA	
	AAAT _	
GAM23	LOC221454 5' AGAGAAGATGAAAGTTG 382	CA AG
	CAGACT TCA CTTCTCT	
	GTTTGA AGT GAAGAGA	
	A_ A_	
GAM23	LOC222444 3' AGAGAAGCCCAGGATGGTC 392	T AA_
	GAC CATC GCTTCTCT	
	CTG GTAG CGAAGAGA	
	— GACC	
GAM23	LOC222962 3' AGAGGGGAGGTAAGTCTG 387	C AAG
	CAGACT ATC CTTCTCT	

GTCTGA TGG GGGGAGA
 A A_

GAM23 LOC245727 5' AGAGAGTGGGGGTGAGTCTG 376 AA_ T
 CAGACTCATC GCT CTCT
 ||||| |||||
 GTCTGAGTGG TGA GAGA
 GGG -

GAM23 LOC253525 5' AGAGAACGCTGCAGGTTG 401 CATCA
 CAGACT AGCTTCTCT
 ||||| |||||||
 GTTTGG TCGAAGAGA
 ACG_

GAM23 LOC254249 5' AGAGAACGTTGAAATTG 397 CTCAT
 CAGA CAAGCTTCTCT
 ||||| |||||||
 GTTT GTTGAAAGAGA
 AAAT_

GAM23 LOC255475 5' AGAGAACGCCGAGCTCTG 403 _ ATCAA
 CAGA CTC GCTTCTCT
 ||||| |||||
 GTCT GAG CGAACAGA
 C C_

GAM23 LOC51026 3' AGAACCCCTTGATGAGACT 146 A C_
 AG CTCATCAAG TTCT
 |||||||||
 TC GAGTAGTTC AAGA
 A CC

GAM23 LOC91308 5' AGAACAGAGATGAGTTG 274 AAG
 CAGACTCATC CTTCT
 ||||| |||||
 GTTTGAGTAG GAAGA
 A_

GAM24 CASP10 3' ATACAACCTGATGTCATATTCC 223 C ____ C_ A III
 ATTTTGGA TG GA AC CAG TTGTA T
 ||||| ||||| |
 AC CT TG GTC AACAT A
 _ TATAC TA C III

GAM24 CASP10 3' ATACAACCTGATGTCATATTCC 224 C ____ C_ A III
 ATTTTGGA TG GA AC CAG TTGTA T
 ||||| ||||| |
 AC CT TG GTC AACAT A
 _ TATAC TA C III

GAM24 CHRN3 5' TTGGGTTCCACTTCGGA 49 A A C
 TCC AA TG GAACCCAG
 ||||| |||||||
 AGG TT AC CTTGGGTT
 C C _

GAM24 LANCL1 3' TACAATCTGGACTTGGTA 100 G C_
 TGC AA CCAGATTGTA
 ||||| |||||||

ATG TT GGTCTAACAT
G CA
GAM24 MS4A3 3' ACATCTGGGTTCAAATTCTG 101 A GC T
CA AAT GAACCCAGAT GT
|| ||| ||||| |||
GT TTA CTTGGGTCTA CA
C AA _
GAM24 SLC1A4 3' TACAATTGTCGGAGTCGCAT 64 CCA_
ATGCGAAC GATTGTA
||||||| |||||
TACGCTTG TTAACAT
ACCCTG
GAM24 ALLC 5' TACAAGGATTCGCATTCTGGG 162 A C_ AGA
TCCA AATGCGAA CC TTGTA
||| ||||| || |||||
GGGT TTACGCTT GG AACAT
C TA _
GAM24 APOL6 3' CTGGGTTCACATTTGGA 206 C
TCCAAAATG GAACCCAG
||||||| |||||
AGGTTTTAC CTTGGGTC
A
GAM24 CBX6 3' TTGGGCTCCATTCTGGA 128 A C A
TCCA AATG GA CCCAG
||||||| |||||
AGGT TTAC CT GGGTT
C _ C
GAM24 FLJ10055 3' TTGGGAGTCCCATTGGGA 156 C A_
TCCAAAATG GA CCCAG
||||||| || |||||
AGGTTTTAC CT GGGTT
C GA
GAM24 FLJ22059 5' CAGTCTGGACCAGCACCTGGGA 191 AA GAAC
TCCAA TGC CCAGATTG
||||| ||| |||||
AGGTT ACG GGTCTGAC
CC ACCA
GAM24 KCNH8 3' TTGGGTTCACATTCTGGA 252 A C
TCCA AATG GAACCCAG
|||||||
AGGT TTAC CTTGGGTT
C A
GAM24 KIAA0870 3' TTGGGCTGCATTGGGA 339 A
TCCAAAATGCG ACCCAG
||||||| |||||
AGGTTTTACGT TGGGTT
C
GAM24 KIAA1157 3' ACAGTATTCCATTGGGA 296 C CCCAG
TCCAAAATG GAA ATTGT
||||||| ||| |||||

		AGGTTTTAC CTT TGACA	
		_ A_	
GAM24	PRO1048	3' ACAATGAGTTGCATTTC 163	C GA
		AAAATGCGAAC CA TTGT	
		TTTTACGTTG GT AACAA	
		A _	
GAM24	PRO1787	3' ACAATTCCGCATTTG 165	AACCCA
		CAAAATGCG GATTGT	
		GTTTACGC TTAACA	
		C_	
GAM24	UBE2G1	3' TACAGATGATTACGCATTTG 67	AACC GA
		CAAAATGCG CA TTGTA	
		GTTTACGC GT GACAT	
		ATTA A_	
GAM24	LOC122402	3' TACTTCTGGTTCACATTTGG 306	C C TT
		A TCCAAAATG GAACC AGA GTA	
		AGGTTTTAC CTTGG TCT CAT	
		A T T_	
GAM24	LOC153592	3' GGAATTTCAGCATTTGGA 355	_ C_
		TCCAAAATGC GAA CC	
		AGGTTTTACG CTT GG	
		A AA	
GAM24	LOC256158	5' ACAATCTGAACGTCTGGG 404	AAAT AACC
		TCCA GCG CAGATTGT	
		GGGT TGC GTCTAACAA	
		C_ AA_	
GAM25	ITGA5	3' CTCAGATCCAGGGACAGAGG 264	GTTAGA A_
		TCTCTG CC GATCTGAG	
		GGAGAC GG CTAGACTC	
		AG_ AC	
GAM25	SF3B3	3' GCTCTAGAACATCTAACCAAGA 116	CCAGA _
		TCTGGTTAGA TCT GAGC	
		AGACCAATCT AGA CTCG	
		A_ T	
GAM25	SLC4A4	3' GCTCAGAGTTGTTAACCAAGA 71	AC A
		TCTGGTTAG CAG TCTGAGC	
		AGACCAATT GTT AGACTCG	
		_ G	
GAM25	ZNF180	3' CTCAGACCTGAATCAGAGA 120	AGAC A
		TCTCTGGTT CAG TCTGAG	

		AGAGACTAA GTC AGACTC	
		_____ C	
GAM25	AP1G2	5' GCCCAGGCACGCCGCCGACCAGAG 233	AGACCAGA A
	A	TCTCTGGTT TCTG GC	
		AGAGACCAG GGAC CG	
		CCCGCAC_ C	
GAM25	BCL2L1	3' GCCCAGATCTGGTCCCTTGAG 241	GTTA_ A
		CTG GACCAGATCTG GC	
		GAC CTGGTCTAGAC CG	
		GTTCC C	
GAM25	FLJ25012	5' CTCAGATCTGAAAAGCACAAGA 250	C _ AGAC
		TCT TG GTT CAGATCTGAG	
		AGA AC CGA GTCTAGACTC	
		_ A AAA_	
GAM25	FLJ31952	3' CAAATCTGGTTCTGAAAG 253	GG _ C
		CT TTAGA CCAGAT TG	
		GA AGTCT GGTCTA AC	
		A_ T A	
GAM25	MDS025	3' CTCAGACCTGGTTGAGATAGA 184	G_ A
		TCTG TTAGACCAG TCTGAG	
		AGAT AGTTGGTC AGACTC	
		AG C	
GAM25	MGC32043	3' GCTCAGATCTGATGCTTCAAGA 249	GGTT AC_
		TCT AG CAGATCTGAGC	
		AGA TC GTCTAGACTCG	
		ACT_ GTA	
GAM25	MSI2	3' CTCCCCATCCCAACCAAGAGA 245	AGACCA CT_
		TCTCTGGTT GAT GAG	
		AGAGACCAA CTA CTC	
		CC_ CCC	
GAM25	ZNF271	5' GCTCAGATCTGGTTAACATCA 395	_ A
		GAGA TCTCTG GTT GACCAGATCTGAGC	
		AGAGAC CAA TTGGTCTAGACTCG	
		TA A	
GAM25	LOC144508	5' GCTCAGATCCATGTGCCAGGGA 362	TAGACCA
		TCTCTGGT GATCTGAGC	
		AGGGACCG CTAGACTCG	
		TGTAC_	
GAM25	LOC145845	3' CTCAAATCCCACCAAGAGA 346	TAGACCA C
		TCTCTGGT GAT TGAG	

		AGAGACCA	CTA ACTC
		CC_____ A	
GAM26	CDH19	3' GAAAATTAAAGGAGCAA	182 A_
		TTGC CTTAAATTTC	
		AACG GAAATTAAAAG	
		AG	
GAM26	CRYGS	5' TGGGAAAACCAGTCTATGCACC	152 T CTTAAA_
		AA TTGGT GCA TTTCCC	
		AACCA CGT AAAAGGGT	
		_ ATCTGACC	
GAM26	CYP1B1	3' GAAAATTGAAAAGTACAACCAA	33 C A_
		TTGGTTG ACTTT AATTTTC	
		AATCAAC TGAAA TTAAAAG	
		AG	
GAM26	GLI3	3' GGAAAAAAAAGACTGCAACCAA	35 C AAA
		TTGGTTGCA TTT TTTTCC	
		AACCAACGT AGA AAAAGG	
		C AA_	
GAM26	PCLO	3' GAAGATAATGCAACCAA	391 CTTTAA
		TTGGTTGCA ATTTTC	
		AACCAACGT TAGAAG	
		AA_	
GAM26	PPP2R5A	3' TGGGAAAGTAAACCAA	102 GC TAAATT
		TTGGTT ACTT TCCCA	
		AACCAA TGAA AGGGT	
		A_	
GAM26	PTER	3' TGAGAAAATTAAAGTGTTCT	207 TT C
		AG TTGG GCACTTAAATTTC CA	
		GATC TGTGAAATTAAAAG GT	
		TT A	
GAM26	RFX5	3' GGGAAAAGCAGTAAACCAA	39 GC TTAAA
		TTGGTT ACT TTTTCCC	
		AACCAA TGA AAAAGGG	
		A_ CG_	
GAM26	CSMD1	3' GGAGTATTAAAGTGGACCAA	301 G ATT
		TTGGTT CACTTAA TTCC	
		AACCAA GTGAAATT GAGG	
		G AT_	
GAM26	MGC15438	3' GAAAGAAAGCGCAGCCAA	220 A AAA
		TTGGTTGC CTTT TTTTC	

		AACCGACG GAAA	GAAAG		
		C	_____		
GAM26	NYD-SP18	3'	GGAGAAAACTGCAACCAA	217	C AAAT
		TTGGTTGCA	TTT	TTTCC	
		AACCAACGT	AAA	AGAGG	
		C	_____		
GAM26	OLFM3	3'	GGAAAAATAATGTAACCAA	340	C TAAA
		TTGGTTGCA	TT	TTTCC	
		AACCAATGT	AA	AAAAGG	
		_____	TA	_____	
GAM26	RPL13A	3'	GGGAAGATGCACAACCAA	115	CACTTTAA
		TTGGTTG	ATTTTCCC		
		AACCAAC	TAGAAGGG		
		ACG	_____		
GAM26	LOC129452	3'	AGAATGGACAAGCGCAACCAA	310	A TAA_
		TTGGTTGC	CTT	ATTTT	
		AACCAACG	GAA	TAAGA	
		C	CAGG		
GAM26	LOC150197	3'	GGATTAAAGTGGAACCAA	335	G ATTT
		TTGGTT	CACTTTAA	TCC	
		AACCAA	GTGAAATT	AGG	
		G	_____		
GAM26	LOC162239	3'	GGAAATTATAATGGCAACCAA	344	AC AAT
		TTGGTTGC	TTTA	TTTCC	
		AACCAACG	AAAT	AAAGG	
		GT	ATT		
GAM26	LOC219972	3'	GAAATGGCAAGTGCAACCAA	379	TAA
		TTGGTTGCACTT	ATTTT		
		AACCAACGTGAA	TAAAG		
		CGG			
GAM27	DDX6	3'	ATTGTGACAAGAATTGTTACC	80	C CCC C
		GG AACGA	CT GTCACAAT		
		CC TTGTT	GA CAGTGTAA		
		A	AA_	A	
GAM27	LOC126917	3'	GCAGTGGGTCTGTTGCCA	309	_ _ C
		TGGCAAC	GACCC	CT GT	
		ACCGTTG	CTGGG	GA CG	
		T	T	_	
GAM27	LOC170395	3'	TATTGTTCTGGGTGTTGCCA	316	G CTCGTC
		TGGCAAC	ACCC	ACAATA	

			ACCGTTG TGGG TGTTAT	
			<u>TCTT</u>	
GAM28	ABCC3	3'	TGCCCTGGCTGTGCTCTAC	170 C A T
			GTG AG ACA CCAGGGCA	
			CAT TC TGT GGTCCCCGT	
			C G C	
GAM28	CASP3	3'	TGCCCTGGATCTACCAGCAT	225 AGAAC_
			GTGC ATCCAGGGCA	
			TACG TAGGTCCCCGT	
			ACCATC	
GAM28	CASP3	3'	TGCCCTGGATCTACCAGCAT	79 AGAAC_
			GTGC ATCCAGGGCA	
			TACG TAGGTCCCCGT	
			ACCATC	
GAM28	EMS1	3'	CCCTGGATCCTCACACTA	90 CA AC
			TAGTG GA ATCCAGGG	
			ATCAC CT TAGGTCCC	
			A_ CC	
GAM28	EMS1	3'	CCCTGGATCCTCACACTA	240 CA AC
			TAGTG GA ATCCAGGG	
			ATCAC CT TAGGTCCC	
			A_ CC	
GAM28	MLLT2	3'	TGCCCTGGACATGTTCTAC	97 CA _
			GTG GAACA TCCAGGGCA	
			CAT TTTGT AGGTCCCCGT	
			CC AC	
GAM28	TACC1	3'	TGCCCCAGATGTTCTGGGCT	104 G _ CA
		G	TAGT CAG AACATC GGGGCA	
			GTCG GTC TTGTAG CCCCGT	
			G C AC	
GAM28	TNFSF6	3'	CCAGGTGTTCTACACTCA	42 T C CA
			A AGTG AGAACATC GG	
			A TCAC TCTGTGG CC	
			C A A_	
GAM28	UBB	3'	TGGCATTACTCTGCACTATA	166 AC_ _
			TATAGTGCAGA ATCCA	
			ATATCACGTCT TA GGT	
			CAT C	
GAM28	AKAP10	3'	TGCCCTTGGATTCTGCACT	113 CA _
			AGTGCAGAA TCCA GGGGCA	

TCACGTCTT AGGT CCCCCGT
 A_ TT
 GAM28 DECR2 3' GCCCCTCTGTCCTGCAC 176 _ TCC
 GTGCAGA ACA AGGGGC
 ||||| |||||
 CACGTCT TGT TCCCCG
 C C_

GAM28 KIAA0240 3' GCCCCTGTGTCCCCTCA 383 CA A TC
 TAGTG GA CA CAGGGGC
 ||||| |||||
 ATCAC CT GT GTCCCCG
 C_ _ _

GAM28 MGC16385 5' GCCCCTGGACGTTCTGCCGC 255 _ _ A
 GTG CAGAA C TCCAGGGGC
 ||||| | |||||
 CGC GTCTT G AGGTCCCCG
 C T C

GAM28 MGC5139 5' GCCCCTGGGCACACTGTA 305 CAGAACAA
 TATAGTG TCCAGGGGC
 ||||| |||||||
 ATGTCAC GGGTCCCCG
 AC_

GAM28 P5-1 3' CCCCTGGATGCCCTAACCACT 110 C_ AA_
 AGTG AG CATCCAGGGG
 ||||| |||||
 TCAC TC GTAGGTCCCC
 CAA CCC

GAM28 TED 3' CCCCTGGGCCCTGCCTA 143 T AACAA
 TAG GCAG TCCAGGGG
 ||||| |||||
 ATC CGTC GGGTCCCC
 _ CC_

GAM28 LOC133418 3' TGCTCTAAAGCTCTGCACTA 311 ACATCCA
 TAGTGCAGA GGGGCA
 ||||| |||||
 ATCACGTCT TCTCGT
 CGAAA_

GAM28 LOC152402 3' GCCCTTACATTCTGCACT 353 CATCC
 AGTGCAGAA AGGGGC
 ||||| |||||
 TCACGTCTT TTCCCCG
 ACA_

GAM28 LOC158677 3' TGCCCCCTGGATATCAGCAATAT 360 G A AC
 A TATA TGC GA ATCCAGGGGCA
 ||||| |||||
 ATAT ACG CT TAGGTCCCCGT
 A A A_

GAM28 LOC221715 3' CCACTGTGCTTGCCTA 390 AA TC _
 TAGTGCAG CA CAG GG
 ||||| |||||

		ATCACGTT GT GTC CC		
		C_ _ A		
GAM28	LOC254746 3'	TGGCATTACTCTGCACTATA	394	AC_ _
		TATAGTGCAGA AT CCA		
		ATATCACGTCT TA GGT		
		CAT C		
GAM28	LOC255098 3'	TGCTCTAAAGCTCTGCACTA	396	ACATCCA
		TAGTGCAGA GGGGCA		
		ATCACGTCT TCTCGT		
		CGAAA_		
GAM29	ADAM19 3'	CTGATGGAGATGCTCAAGGC	228	AG TATGG
		GCCTT GCATCTCC CAG		
		CGGAA CGTAGAGG GTC		
		CT TA_		
GAM29	LFG 3'	TGCCACAGGCCCTAACCGCT	319	ATCTC A
		AGCCTTAGGC CT TGGCA		
		TCGGAATCCG GA ACCGT		
		C		
GAM29	NOLA2 5'	GGAAGTGATGCCTAACAGCT	393	C _
		AGC TTAGGCATC TCC		
		TCG AATCCGTAG AGG		
		A TGA		
GAM29	FLJ10751 3'	CCAGAGACACCTGAGGC	158	CA CTA
		GCCTTAGG TCTC TGG		
		CGGAGTCC AGAG ACC		
		AC _		
GAM29	FLJ10751 3'	CCAGAGACACCTGAGGC	159	CA CTA
		GCCTTAGG TCTC TGG		
		CGGAGTCC AGAG ACC		
		AC _		
GAM29	FLJ10925 5'	CTGCCCCCAGGGACACCTAAGG	160	CA T AT_
		C GCCTTAGG TC CCT GGCAG		
		CGGAATCC AG GGA CCGTC		
		AC _ CCC		
GAM29	KIAA1118 3'	GTGGTTGAGATGCCACGGCT	289	TTA CT G
		AGCC GGCATCTC AT GC		
		TCGG CCGTAGAG TG TG		
		CAC T_ G		
GAM29	KIAA1649 3'	CTGCCATTCTGTGCCTAGGCT	215	T CTCCT
		AGCCT AGGCAT ATGGCAG		

TCGGA TCCGTG TACCGTC
 - TCTT_
 GAM29 LIMR 3' CTGCCATCTGCCTGCCTAGGC 157 T TCTCCT
 GCCT AGGCA ATGGCAG
 ||||| |||||
 CGGA TCCGT TACCGTC
 - CGTC_

GAM29 MGC14161 5' CCAGAGAGATGCCAAAGGC 221 A CTA
 GCCTT GGCATCTC TGG
 ||||| ||||| III
 CGGAA CCGTAGAG ACC
 A AG_

GAM29 NJMU-R1 3' CATGAAGAAATGCCTGAAGC 188 C C C_
 GC TTAGGCAT TC TATG
 ||||| ||||| II III
 CG AGTCCGTA AG GTAC
 A A AA

GAM29 SEMA3E 3' CTGTTGTGAGAAATGCCAGGC 119 TA C C TG
 T AGCCT GGCAT TC TA GCAG
 ||||| ||||| II || III
 TCGGA CCGTA AG GT TGTC
 C_ A A GT

GAM29 YKT6 3' CTGCCATAGATAACCCTAAC 106 CATCTC
 CTTAGG CTATGGCAG
 ||||| |||||
 GAATCC GATACCGTC
 CATA_

GAM29 LOC142972 5' GCCACAGGAGATGCCAAAGC 271 C A A
 GC TT GGCATCTCCT TGGC
 ||||| ||||| III
 CG AA CCGTAGAGGA ACCG
 A C C

GAM29 LOC143689 3' TGCCATAAGCTCAAGGCT 318 AG ATCTCC
 AGCCTT GC TATGGCA
 ||||| II |||||
 TCGGAA CG ATACCGT
 CT A_

GAM29 LOC148930 5' CCATAGGGAGCCTAAC 332 A T
 CTTAGGC TC CCTATGG
 ||||| |||||
 GAATCCG AG GGATACC

--
 GAM29 LOC220469 3' CCAAGGGATGCCAAAGC 317 C A T A
 GC TT GGCATC CCT TGG
 ||||| ||||| III |||
 CG AA CCGTAG GGA ACC
 A C _ _

GAM29 LOC253782 3' CATAAGAGCACCTAAC 398 CAT C
 GCCTTAGG CTC TATG
 ||||| III |||

CGGAATCC GAG ATAC
AC_ A
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